

SEQUENCE LISTING

<110> Roch, Jean-Marc
 Bartel, Paul L.
 Reichman, Karen

<120> Protein-Protein Interactions in Neurodegenerative Diseases

<130> Protein Interactions in ND

<140>
 <141>

<150> US 60/240,790
 <151> 2000-10-17

<160> 4

<170> PatentIn Ver. 2.0

<210> 1
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:tail for forward primer for yeast two-hybrid system

<400> 1
 gcaggaaaca gctatgacca tacagtcagc ggccgccacc 40

<210> 2
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:tail for reverse primer for yeast two-hybrid system

<400> 2
 acggccagtc gcgtggagtg ttatgtcatg cgcccgcta 39

<210> 3
 <211> 2740
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (217)..(1332)

<400> 3
 cgagaatttc cagcaggcaa ggcagtggcc gctttgactg cttgcttcgg agatccgaga 60
 cgacggagaa ggcactotta ttaccgacc aagaaagctc ctcccgcgtc ctccgttagc 120
 taattaaaaac atttttcagc gacgtagcca tccagagaca ttccattatt gttccattga 180
 cctttccctc atcaetgagt cctttggagc tgagtt atg tca aca gct gcc tta 234

0975072 "1034"

Met Ser Thr Ala Ala Leu
1 5

att act ttg gtc aga agt ggt ggg aac cag gtg aga agg aga gtg ctg	282
Ile Thr Leu Val Arg Ser Gly Gly Asn Gln Val Arg Arg Arg Val Leu	
10 15 20	
cta agc tcc cgc ctg ctg cag gac gac agg cgg gtg aca ccc acg tgc	330
Leu Ser Ser Arg Leu Leu Gln Asp Asp Arg Arg Val Thr Pro Thr Cys	
25 30 35	
cac agc tcc act tca gag cct agg tgt tct cgg ttt gac cca gat ggt	378
His Ser Ser Thr Thr Glu Pro Arg Cys Ser Arg Phe Asp Pro Asp Gly	
40 45 50	
agt ggg agt cca gct acc tgg gac aat ttt ggg atc tgg gat aac cgc	426
Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe Gly Ile Trp Asp Aac Arg	
55 60 65 70	
att gat gag cca att ctg ctg cca ccc agc att aag tat ggc aag cca	474
Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser Ile Lys Tyr Gly Lys Pro	
75 80 85	
att ccc aaa atc agc ttg gaa aat gtg ggg tgc gcc tca cag att ggc	522
Ile Pro Lys Ile Ser Leu Glu Asn Val Gly Cys Ala Ser Gln Ile Gly	
90 95 100	
aaa cgg aaa gag aat gaa gat cgg ttt gac ttc gct cag ctg aca gat	570
Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp Phe Ala Gln Leu Thr Asp	
105 110 115	
gag gtc ctg tac ttt gca gtg tat gat gga cac ggt gga cct gca gca	618
Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly His Gly Gly Pro Ala Ala	
120 125 130	
gct gat ttc tgt cat acc cac atg gag aaa tgt att atg gat ttg ctt	666
Ala Asp Phe Cys His Thr His Met Glu Lys Cys Ile Met Asp Leu Leu	
135 140 145 150	
cct aag gag aag aac ttg gaa act ctg ttg acc ttg gct ttt cta gaa	714
Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu Thr Leu Ala Phe Leu Glu	
155 160 165	
ata gat aaa gcc ttt tgc agt cat gcc cgc ctg tct gct gat gca act	762
Ile Asp Lys Ala Phe Ser Ser His Ala Arg Leu Ser Ala Asp Ala Thr	
170 175 180	
ctt ctg acc tct ggg act act gca aca gta gcc cta ttg cga gat ggt	810
Leu Leu Thr Ser Gly Thr Thr Ala Thr Val Ala Leu Leu Arg Asp Gly	
185 190 195	
att gaa ctg gtt gta gcc agt gtt ggg gac agc cgg gct att ttg tgt	858
Ile Glu Leu Val Val Ala Ser Val Gly Asp Ser Arg Ala Ile Leu Cys	
200 205 210	
aga aaa gga aaa ccc atg aag ctg acc att gac cat act cca gaa aga	906
Arg Lys Gly Lys Pro Met Lys Leu Thr Ile Asp His Thr Pro Glu Arg	
215 220 225 230	
aaa gat gaa aaa gaa agg atc aag aaa tgt ggt ggt ttt gta gct tgg	954
Lys Asp Glu Lys Glu Arg Ile Lys Lys Cys Gly Gly Phe Val Ala Trp	
235 240 245	
aat agt ttg ggg cag cct cac gta aat ggc agg ctt gca atg aca aga	1002

00975072 22031304

Asn Ser Leu Gly Gln Pro His Val	Asn Gly Arg Leu Ala Met Thr Arg	
250	255	260
agt att gga gat ttg gac ctt aag acc agt ggt gtc ata gca gaa cct	1050	
Ser Ile Gly Asp Leu Asp Leu Lys	Thr Ser Gly Val Ile Ala Glu Pro	
265	270	275
gaa act aag agg att aag tta cat cat gct gat gac agc ttc ctg gtc	1098	
Glu Thr Lys Arg Ile Lys Leu His His Ala Asp	Asp Ser Phe Leu Val	
280	285	290
ctc acc aca gat gga att aac ttc atg gtg aat agt caa gag att tgt	1146	
Leu Thr Thr Asp Gly Ile Asn Phe Met Val Asn	Ser Gln Glu Ile Cys	
295	300	305
gac ttt gtc aat cag tgc cat gat ccc aac gaa gca gcc cat gcg gtg	1194	
Asp Phe Val Asn Gln Cys His Asp Pro Asn Glu Ala Ala His Val		
315	320	325
act gaa cag gca ata cag tac ggt act gag gat aac agt act gca gta	1242	
Thr Glu Gln Ala Ile Gln Tyr Gly Thr Glu Asp Asn Ser Thr Ala Val		
330	335	340
gta gtg cct ttt ggt gcc tgg gga aaa tat aag aac tct gaa atc aac	1290	
Val Val Pro Phe Gly Ala Trp Gly Lys Tyr Lys Asn Ser Glu Ile Asn		
345	350	355
ttc tca ttc agc aga agc ttt gcc tcc agt gga cga tgg gcc	1332	
Phe Ser Phe Ser Arg Ser Phe Ala Ser Ser Gly Arg Trp Ala		
360	365	370
tgattaccag ctgggactta gagtttctgt gcaacagttt ttcactgagc atgtcaagaa	1392	
actgataaga tcaaaaaggt.ctcctaactc actagatcag cgcacaagto agtgtaaacc	1452	
acttagatag tagttttttc ataaatgctc atcatatttta tgttccgctg tacatgttca	1512	
gtataaatat atgtgtagtg aagctactgt gagtctttaa atggaaagag caaatgagaa	1572	
gtggtttgga tacacttgat gagagatgag agtgtcacat taataatttt taagactctt	1632	
aggcagctat gggtttcttt tgatcatttt tgttctttat tcattttgaac acgtttttga	1692	
agttcttcaa aactagtcag ttggaatttt gacagctatt caatatgtga tctccaaagt	1752	
taaaaaaatt tttttccaga cttccctaata cctaaaaatgc gagtttttat ttttaataac	1812	
tgtaccaagg aataagtatg aaaacagttc tctgtttacca tatttttgat tctggaccac	1872	
ttactgggtga aagcaacctg gcaaaagaaa ttaattttggc caggcacagt ggctcatgcc	1932	
tgtaatccca aattgctggg attacagcac tgtgccctcc taggaaatta ttttttaagt	1992	
gaaattttat ttttattttt tttaggattt tggtagagaa tgagtaggcc tactcatcaa	2052	
tatcaaacag gacatttagt tcttttctctt agaacagaca taaattttaa ttcattggtaa	2112	
tatgataata agaaaaatgct tctatttttc tttagcacct ccatggttct catataccca	2172	
tgtctgtaaa aagtgcactg agaattttgt tgggtttacat tttattgtat ttattagatt	2232	
cgcttatata gatgacttag gcagaaataa agtcatgtct ttagaagggtg aacaagccaa	2292	
cttgtgatgg cctgcctttt gcttttggca gttgggatga gaacaattga ctctccatt	2352	

0975072 = 6333

ggtgtttaga tagttgaaat ggtgcgttgg tggtcatact tagtgttcta ggctgtgaaa 2412
 tcatggagatt cttccacttc caagaatgac tcatttgcgt ttggattcta gtacagaatt 2472
 tagcagcctg atgtgtcccc aaactgattt aatttctact gaagtgcctt tgtgtacatt 2532
 tgttttgtaa ttaccaaaag tactacctga gtgtataatg actcctgcag tgagttaatg 2592
 taattgtgcg tttagaccatt gttttaaatc tgtgtactag agtaactgtg agcagaatga 2652
 aatcacatta tctcagtggt caaaatatca ttctaataaa gtacatgcat taaacaattt 2712
 taaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2740

<210> 4
 <211> 372
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Ser Thr Ala Ala Leu Ile Thr Leu Val Arg Ser Gly Gly Asn Gln
 1 5 10 15
 Val Arg Arg Arg Val Leu Leu Ser Ser Arg Leu Leu Gln Asp Arg
 20 25 30
 Arg Val Thr Pro Thr Cys His Ser Ser Thr Ser Glu Pro Arg Cys Ser
 35 40 45
 Arg Phe Asp Pro Asp Gly Ser Gly Ser Pro Ala Thr Trp Asp Asn Phe
 50 55 60
 Gly Ile Trp Asp Asn Arg Ile Asp Glu Pro Ile Leu Leu Pro Pro Ser
 65 70 75 80
 Ile Lys Tyr Gly Lys Pro Ile Pro Lys Ile Ser Leu Glu Asn Val Gly
 85 90 95
 Cys Ala Ser Gln Ile Gly Lys Arg Lys Glu Asn Glu Asp Arg Phe Asp
 100 105 110
 Phe Ala Gln Leu Thr Asp Glu Val Leu Tyr Phe Ala Val Tyr Asp Gly
 115 120 125
 His Gly Gly Pro Ala Ala Ala Asp Phe Cys His Thr His Met Glu Lys
 130 135 140
 Cys Ile Met Asp Leu Leu Pro Lys Glu Lys Asn Leu Glu Thr Leu Leu
 145 150 155 160
 Thr Leu Ala Phe Leu Glu Ile Asp Lys Ala Phe Ser Ser His Ala Arg
 165 170 175
 Leu Ser Ala Asp Ala Thr Leu Leu Thr Ser Gly Thr Thr Ala Thr Val
 180 185 190
 Ala Leu Leu Arg Asp Gly Ile Glu Leu Val Val Ala Ser Val Gly Asp
 195 200 205
 Ser Arg Ala Ile Leu Cys Arg Lys Gly Lys Pro Met Lys Leu Thr Ile
 210 215 220

Asp His Thr Pro Glu Arg Lys Asp Glu Lys Glu Arg Ile Lys Lys Cys
 225 230 235 240
 Gly Gly Phe Val Ala Trp Asn Ser Leu Gly Gln Pro His Val Asn Gly
 245 250 255
 Arg Leu Ala Met Thr Arg Ser Ile Gly Asp Leu Asp Leu Lys Thr Ser
 260 265 270
 Gly Val Ile Ala Glu Pro Glu Thr Lys Arg Ile Lys Leu His His Ala
 275 280 285
 Asp Asp Ser Phe Leu Val Leu Thr Thr Asp Gly Ile Asn Phe Met Val
 290 295 300
 Asn Ser Gln Glu Ile Cys Asp Phe Val Asn Gln Cys His Asp Pro Asn
 305 310 315 320
 Glu Ala Ala His Ala Val Thr Glu Gln Ala Ile Gln Tyr Gly Thr Glu
 325 330 335
 Asp Asn Ser Thr Ala Val Val Val Pro Phe Gly Ala Trp Gly Lys Tyr
 340 345 350
 Lys Asn Ser Glu Ile Asn Phe Ser Phe Ser Arg Ser Phe Ala Ser Ser
 355 360 365
 Gly Arg Trp Ala
 370

0075072-104304